

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd

OM protein - protein search, using sw model

Run on: January 16, 2003, 16:40:12 / Search time: 18.2143 seconds
(without alignments)
56.562 Million cell updates/sec

Title: US-09-856-070-26
Perfect score: 28
Sequence: 1 Q9H45

Scoring table: BLASTM52
Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: 1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organello:
9: sp_phage:
10: sp_plant:
11: sp_protein:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_virus:
16: sp_bacteriophage:
17: sp_archaea:

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Query No.	Score	Match	Length	DB ID	Description
1	28	100.0	106	4	Q9H44	Q9H44 homo sapien
2	28	100.0	125	5	Q4212	Q4212 bradylab
3	28	100.0	130	16	Q9K660	Q9K660 bacillus ha
4	28	100.0	156	16	Q9K011	Q9K011 bacillus ha
5	28	100.0	171	2	Q50138	Q50138 ruminococ
6	28	100.0	179	5	Q95P73	Q95P73 baenatelia
7	28	100.0	263	16	Q97NV2	Q97NV2 streptococ
8	28	100.0	260	1	Q97700	Q97700 streptococ
9	28	100.0	315	13	Q03292	Q03292 xenopus lac
10	28	100.0	361	16	Q97744	Q97744 streptococ
11	28	100.0	370	12	Q9P217	Q9P217 xestia c-ni
12	28	100.0	376	5	Q955W7	Q955W7 caenorhabdi
13	28	100.0	400	5	Q9VFC9	Q9VFC9 drosophila
14	28	100.0	404	5	Q8T0T3	Q8T0T3 drosophila
15	28	100.0	406	11	Q90TK3	Q90TK3 rattus norv
16	28	100.0	443	16	Q24532	Q24532 volvox cart

17	28	100.0	451	12	Q66453	Q66453 duvenhage v
18	28	100.0	469	17	Q9H4T1	Q9H4T1 thermoplasm
19	28	100.0	491	2	Q9ANR4	Q9ANR4 bradyrhizob
20	28	100.0	505	11	Q8R4Z5	Q8R4Z5 mus musculu
21	28	100.0	512	8	Q98S92	Q98S92 quillardia
22	28	100.0	568	10	Q65590	Q65590 arabidopsis
23	28	100.0	576	10	Q9C9A7	Q9C9A7 arabidopsis
24	28	100.0	596	4	Q9C2H4	Q9C2H4 homo sapien
25	28	100.0	651	10	Q9C9S7	Q9C9S7 arabidopsis
26	28	100.0	675	2	Q522B8	Q522B8 acrobacteri
27	28	100.0	700	16	Q9K679	Q9K679 bacillus ha
28	28	100.0	824	4	Q8T0K3	Q8T0K3 homo sapien
29	28	100.0	825	11	Q8K4Z6	Q8K4Z6 mus musculu
30	28	100.0	833	19	Q9J0K2	Q9J0K2 arabidopsis
31	28	100.0	961	10	Q9M4T4	Q9M4T4 arabidopsis
32	28	100.0	961	10	Q8W4N3	Q8W4N3 arabidopsis
33	28	100.0	1188	10	Q9LNU5	Q9LNU5 arabidopsis
34	28	100.0	1332	11	Q8VHV9	Q8VHV9 mus musculu
35	28	100.0	1333	6	Q9WNH5	Q9WNH5 cryotolagus
36	28	100.0	1333	11	Q8VHU5	Q8VHU5 mus musculu
37	28	100.0	4621	11	Q8VHE6	Q8VHE6 mus musculu
38	28	100.0	4624	4	Q8TE73	Q8TE73 homo sapien
39	25	89.3	54	4	Q9JNK5	Q9JNK5 homo sapien
40	25	89.3	65	16	Q9PAJ6	Q9PAJ6 xyliella fas
41	25	89.3	83	10	Q9M445	Q9M445 cicier ariet
42	25	89.3	90	16	Q9P7H0	Q9P7H0 xyliella fas
43	25	89.3	92	10	Q9SP60	Q9SP60 arabidopsis
44	25	89.3	93	10	Q8VWV8	Q8VWV8 malus domes
45	25	89.3	97	16	Q9WZG3	Q9WZG3 thermotoga

ALIGNMENTS

RESULT 1

Q9H4N4	PRELIMINARY;	PRT;	106 AA.
AC Q9H4N4			
DT 01-MAR-2001 (TREMREL. 16, Created)			
DT 01-MAR-2001 (TREMREL. 16, Last sequence update)			
DT 01-MAR-2001 (TREMREL. 16, Last annotation update)			
DE Clone Q9H4N4 mRNA sequence.			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX NCBI_TaxID=9606;			
RN [1]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=95567227; PubMed=8513474;			
RA Andersson B., Wentland M.A., Kitzfrense J.Y., Liu W., Gibbs K.A.;			
PT "A double adaptor method for improved shotgun library			
PT construction."			
RL Anal. Biochem. 236:107-113(1996).			
RN [2]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=97264341; PubMed=9110174;			
RA Yu W., Anderson B., Worley K.C., Muzny D.M., Ding Y., Liu W.,			
RA Poirault J.Y., Wentland M.A., Lennon G., Gibbs R.A.;			
RI Genome Res. 7:353-358(1997)			
RN [3]			
RP SEQUENCE FROM N.A.			
RA Zhou J., Yu W., Tang H., Mei G., Tsang Y.T.M., Bouck J., Gibbs R.A.;			
RA MacCallum J.F.;			
RI S. Smith (J. Mol. Biol. 2000) in the EMBL/GenBank/Tran databases.			
OR EMBL, AY307145, AAC02031.1;			
SV SEQUENCE 106 AA; 13211 MW; 80A5559A8209DE25 CRC64;			

Query Match 100.0% Score 28; DB 4; Length 106;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Q9 1 Q9H45

Query Match:	100.00;	Score: 28;	DB: 2;	Length: 171;
Best Local Similarity	100.00;	Pred. No.:	1e+02;	

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDYE 5
|||||

Db 71 QDYE 75

RESULT 6

Q95P73 PRELIMINARY: PRT: 179 AA.

AC Q95P73: (1-DEC-2001 (TrEMBLrel. 19, Created))

DI 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DI 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Thrombostasin (Fragment).

OS Haematobia irritans (horn fly).

OC Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta;

OC Pterygota; Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha;

OC Muscidae; Muscidae; Haematobia.

OX NCBI_TaxID=7368;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-SALIVARY GLAND;

RA Zhang D., Cupp M.S., Cupp F.W.

RT "thrombostasin: a novel anti-thrombin protein purified from horn fly saliva.";

RL Insect Biochem Mol Biol 0:0-0(2001)

FT EMBL: AF260078; AAK60131; -

FT NON_TER 1

SQ SEQUENCE 179 AA, 19910 MW, 46710ARRAIAIKHFA CRG64.

Query Match 100.0%; Score 28; Len 5; Length 179;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDYE 5
|||||

Db 87 QDYE 91

RESULT 7

Q97NV2 PRELIMINARY: PRT: 253 AA.

AC Q97NV2: (1-OCT-2001 (TrEMBLrel. 13, Created))

DI 01-OCT-2001 (TrEMBLrel. 13, Last sequence update)

DI 01-OCT-2001 (TrEMBLrel. 13, Last annotation update)

DE Oxidoreductase, short chain dehydrogenase/reductase family.

GN SP1909.

OS Streptococcus pneumoniae.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;

OC Streptococcaceae; Streptococcus.

OX NCBI_TaxID=1313;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-TIGR4;

RX MEDLINE=21357209; PubMed=11463916;

RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.P.,
Peterson S., Heidelberg J., DeBoy P.T., Haft D.H., Dodson P.J.,
Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.L.,
Umayam L.A., White O., Salzberg S.L., Lewis M.F., Padine B.,
Holtzapple E., Khouri H., Wolf A.M., Interback T.R., Hansen C.L.,
McDonald L.A., Feldblyum T.V., Anquilli S., Dickinson T., Hickey E.K.,
Holt I.E., Loftis B.J., Yang F., Smith H.O., Venter J.C.,
Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RT "Complete genome sequence of a virulent isolate of Streptococcus pneumoniae.";

RL Science 293:498-506(2001).

DF EMBL: AE007482; AAK75978; -

DB TIGR: SP1909;

DR InterPro: IPR002198; ADH_short; 1.

DR Pfam: PF00106; adh_short; 1.

DR PRINTS: PR00080; SDRFAMILY.

HP PROSITE: PS00061; ADH_SHORT; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 253 AA; 27455 MW; F6B2F1753G57181D CRG64;

Query Match 100.0%; Score 28; Len 16; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDYE 5
|||||

Db 99 QDYE 103

RESULT 8

Q9F700 PRELIMINARY: PRT: 260 AA.

AC Q9F700: (1-MAR-2001 (TrEMBLrel. 16, Created))

DI 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DI 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Putative oxidoreductase.

OS Streptococcus thermophilus.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;

OC Streptococcaceae; Streptococcus.

OX NCBI_TaxID=1308;

RN [1]

RP SEQUENCE FROM N.A.

RC MEDLINE=20455572; PubMed 19983327;

RA Lucchini S., Sidoti J., Brussow H.

RT "Broad-range bacteriophage resistance in Streptococcus thermophilus by insertional mutagenesis.";

RL Virology 275:257-277(2000).

CC -1- SIMILARITY: REFIONS TO THE SHIPT-HAIN PEPYD-GENASES/PEPOTASES (SDR) FAMILY.

DP EMBL: AF288038; AAG22016; 1; -

DR InterPro: IPR002198; ADH_short.

DR Pfam: PF00106; adh_short; 1.

DR PRINTS: PR00080; SDRFAMILY.

DR PROSITE: PS00061; ADH_SHORT; UNKNOWN_1.

KW Oxidoreductase.

SQ SEQUENCE 260 AA; 29120 MW; BD45DFBDEB12CB21 CRG64;

Query Match 100.0%; Score 28; Len 2; Length 260;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDYE 5
|||||

Db 104 QDYE 108

RESULT 9

Q03292 PRELIMINARY: PRT: 315 AA.

AC Q03292: (1-NOV-1996 (TrEMBLrel. 01, Created))

DI 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DI 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

DE Animal 4 (Xian4).

OS Xenopus laevis (African clawed frog).

OC Pterygota, Metazoa, Chordata, Grenata, Vertebrata, Batrachostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;

OC Xenopodidae; Xenopus.

OX NCBI_TaxID=8355;

RN [1]

RP SEQUENCE FROM N.A.

RC MEDLINE=93187758; PubMed=1284029;

RA Keddy H.A., Kloc M., Etkin L.D.

RT "The cloning and characterization of a localized maternal transcript in Xenopus laevis whose zygotic counterpart is deleted in the CNS.";

PL Mech Dev 39:143-150(1992)

CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.

DR EMBL: M94969; AAA73357.1; -

```

DR HSSP: P27986; IPHT.
DR InterPro: IPR001452; SH3.
DR Pfam: PF00019; SH3; 1.
DR PRINTS: PR00452; SH3DOMAIN.
DR PRODOM: PD000066; SH3; 1.
DR SMART: SM00426; SH3; 1.
DR PROSITE: PS00002; SH3; 1.
KW SH3 domain.
SQ SEQUENCE 315 AA; 34257 MW; A517E2FC0AF017AF CRC64;

Query Match 100.0%; Score 28; DB 13; Length 315;
Best local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDVEE 5
DB 226 QDVEE 230

RESULT 10
Q97RA4 PRELIMINARY; PRT; 361 AA.
AC Q97RA4;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical protein SP0921.
GN SP0921.
OS Streptococcus pneumoniae
OC Bacteria; Firmicutes; Bacillus/Clostridium group, Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-TIGR4;
RX MEDLINE-21357209; PubMed-11463916;
RA Terrill H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
RA Burkett A.S., Gwinn M., Kolonay J.F., Nelson W.C., Petersen J.P.,
RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
RA Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
RA McDonald L.A., Feldblyum T.V., Anglucci S., Dickinson T., Hickey E.K.,
RA Holt I.E., Lolius B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RI "Complete genome sequence of a virulent isolate of Streptococcus
RI pneumoniae."
RL Science 293:498-506(2001).
DR EMBL: AE007397; AAK75045.1; -.
DR TIGR: SP0921; -.
KW Hypothetical protein, Complete proteome.
SQ SEQUENCE 361 AA; 40341 MW; HPEEAPB3F0773250 CRC64;

Query Match 100.0%; Score 28; DB 16; Length 361;
Best local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDVEE 5
DB 124 QDVEE 127

RESULT 11
Q9PZ17 PRELIMINARY; PRT; 370 AA.
AC Q9PZ17;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE OMF26.
OS Xestia c-nigrum granulosis virus (XcGV) (Xestia c-nigrum
OC granulovirus).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus.
OX NCBI_TaxID=51677;

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-99434230; PubMed-10502508;
RA Hayakawa T., Ko R., Okano K., Seong S.L., Goto C., Maeda S.;
RT "Sequence analysis of the Xestia c-nigrum granulovirus genome.";
PL Virology 262:277-287(1999)
DR EMBL: AF162221; AAF05140.1; -.
SQ SEQUENCE 370 AA; 42913 MW; 4EFD1A45F050CE84 CRC64;

Query Match 100.0%; Score 28; DB 12; Length 370;
Best local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDVEE 5
DB 151 QDVEE 155

RESULT 12
Q95QW7 PRELIMINARY; PRT; 376 AA.
AC Q95QW7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 44.4 kDa protein.
GN C14F5.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Pseudorhinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE-99069613; PubMed-9851916;
RA None;
PT "Genome sequence of the nematode C. elegans: a platform for
PT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 284:212-218(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN BRISTOL N2;
RX Minx P.;
RT "The sequence of C. elegans cosmid C14F5.";
RI Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX Waterston R.;
RT "Direct Submission.";
RI Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: U29082; AAL02434.1; -.
KW Hypothetical protein.
SQ SEQUENCE 376 AA; 44436 MW; 53E3255B13C4A6CE CRC64;

Query Match 100.0%; Score 28; DB 5; Length 376;
Best local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDVEE 5
DB 99 QDVEE 103

RESULT 13
Q9VFC9 PRELIMINARY; PRT; 400 AA.
AC Q9VFC9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE CG3987 protein.
GN CG3987.

```

OS Drosophila melanogaster (fruit fly);
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila;
 OX NCBI_TaxID=7227;
 RN [1]

PP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RA Adams M.D., Gelniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amandites P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.F., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.P., Vandal M.D., Zhang Q., Chen L.X.,
 RA Brandon P.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Brill J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin B.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova P., Botchan M.P., Bouck J., Brokstein P., Brotlier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos R., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Douc I.E., Downes M., Dugan-Rocha S., Durkin B.C., Dunn P.,
 RA Durbin K.T., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodzik A., Gong F., Gorell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Hatvey D., Heiman T.J., Hernandez J.R., Hoek J.,
 RA Hostin D., Houston K.A., Howland T.L., Wei M.-H., Ibeagwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel R.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levinson A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy R., Murphy J., Murny D.M., Nelson D.I.,
 RA Nelson D.R., Nelson K.A., Nixon K.A., Nusskern D.R., Pauley J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier F., Spradling A.C., Stapleton M., Strong R., Sun F.,
 RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman C.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Wodage J., Worley K.C., Wu D., Yang S., Yao A.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao X., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,
 RA Gibbs K.A., Myers E.W., Rubin G.M., Venter J.;
 RT "The genome sequence of Drosophila melanogaster."
 FI Science 287:2185-2195(2000)
 DR EMBL: AE004707; AAF51411;
 DR FlyBase: FBgn0038292; CG3987;
 SQ SEQUENCE 400 AA; 45634 MW; 3B7A8C55327B353C CRC64;

Query Match 100.0%; Score 28; DB 5; Length 400;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYEE 5
 DB 44 QYEE 48
 |||||

RESULT 14

Q8T0T3 PRELIMINARY; PPT: 404 AA;
 AC Q8T0T3;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE GH09123p.
 GN CG3987.
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila

OX NCBI_TaxID=7227;
 RN [1]
 RE SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorset V., Parfian D., Frise E., George P.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.T.,
 RA Ninola J., Pavl-b J., Parojas V., Park S., Phuan-uavong S., Wan K.,
 RA Yu C., Lewis S.F., Rubin G.M., Celniker S.;
 PL Submitted (Dec-2001) to the EMBL/GenBank/DBJ databases
 DR EMBL: AY069074; AAL39219.1; -;
 SQ SEQUENCE 404 AA; 46060 MW; 2E305852FEF9315R CRC64;

Query Match 100.0%; Score 28; DB 5; Length 404;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYEE 5
 DB 48 QYEE 52
 |||||

RESULT 15

Q9JIK3 PRELIMINARY; PPT: 406 AA;
 IN Q9JIK3
 AC Q9JIK3;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Regulator of steroidogenic factor 1 (Fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RE SEQUENCE FROM N.A.
 RC STRAIN=SPAGNE-DAWLEY; TISSUE=OVARY;
 RX MEDLINE=20581305; PubMed=11145740;
 RA Ou Q., Mouillet J.-F., Yan X., Dorn C., Crawford P.A., Sadovsky Y.;
 RT "The hFAB Box Protein DP103 Is a Regulator of Steroidogenic Factor-1";
 PL Mol. Endocrinol. 15:69-74(2001)
 DR EMBL: AF230455; AAF76302.1; -;
 FT NON-ITER 1
 SQ SEQUENCE 406 AA; 45591 MW; 40P0260849886807 CRC64;

Query Match 100.0%; Score 28; DB 11; Length 406;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYEE 5
 DB 353 QYEE 357
 |||||

Search completed: January 16, 2003, 16:55:49

Job time : 20.2143 secs

